



SEQUENCE LISTING

<110> Chan, Doug W
Chen, Ping-Chi B
Chen, David J

<120> DNA Dependent Protein Kinase Catalytic Subunit Phosphorylation Sites and Antibodies Thereto

<130> IB-1807 PCT

<140> US 10/511,561

<141> 2004-10-15

<150> US 60/375,094

<151> 2002-04-22

<160> 28

<170> PatentIn version 3.1

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Gln Leu Ile Arg Gly Leu Gly Gln Glu Cys Val Leu Ser Ser Ser Pro
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Ala Val Leu Ala Leu Gln Thr Ser Leu Val Phe Ser Arg Asp Phe Gly
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Leu Leu Val Phe Val Arg Lys Ser Leu Asn Ser Ile Glu Phe Arg Glu
65 70 75 80

Cys Arg Glu Glu Ile Leu Lys Phe Leu Cys Ile Phe Leu Glu Lys Met
85 90 95

Gly Gln Lys Ile Ala Pro Tyr Ser Val Glu Ile Lys Asn Thr Cys Thr
100 105 110

Ser Val Tyr Thr Lys Asp Arg Ala Ala Lys Cys Lys Ile Pro Ala Leu
115 120 125

Asp Leu Leu Ile Lys Leu Leu Gln Thr Phe Arg Ser Ser Arg Leu Met
130 135 140

Asp Glu Phe Lys Ile Gly Glu Leu Phe Ser Lys Phe Tyr Gly Glu Leu
145 150 155 160

Ala Leu Lys Lys Lys Ile Pro Asp Thr Val Leu Glu Lys Val Tyr Glu
165 170 175

Leu Leu Gly Leu Leu Gly Glu Val His Pro Ser Glu Met Ile Asn Asn
180 185 190

Ala Glu Asn Leu Phe Arg Ala Phe Leu Gly Glu Leu Lys Thr Gln Met
195 200 205

Thr Ser Ala Val Arg Glu Pro Lys Leu Pro Val Leu Ala Gly Cys Leu
210 215 220

Lys Gly Leu Ser Ser Leu Leu Cys Asn Phe Thr Lys Ser Met Glu Glu
225 230 235 240

Asp Pro Gln Thr Ser Arg Glu Ile Phe Asn Phe Val Leu Lys Ala Ile
245 250 255

Arg Pro Gln Ile Asp Leu Lys Arg Tyr Ala Val Pro Ser Ala Gly Leu
260 265 270

Arg Leu Phe Ala Leu His Ala Ser Gln Phe Ser Thr Cys Leu Leu Asp
275 280 285

Asn Tyr Val Ser Leu Phe Glu Val Leu Leu Lys Trp Cys Ala His Thr
290 295 300

Asn Val Glu Leu Lys Lys Ala Ala Leu Ser Ala Leu Glu Ser Phe Leu
305 310 315 320

Lys Gln Val Ser Asn Met Val Ala Lys Asn Ala Glu Met His Lys Asn
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Lys Leu Gln Tyr Phe Met Glu Gln Phe Tyr Gly Ile Ile Arg Asn Val
340 345 350

Asp Ser Asn Asn Lys Glu Leu Ser Ile Ala Ile Arg Gly Tyr Gly Leu
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Phe Ala Gly Pro Cys Lys Val Ile Asn Ala Lys Asp Val Asp Phe Met
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Tyr Val Glu Leu Ile Gln Arg Cys Lys Gln Met Phe Leu Thr Gln Thr
385 390 395 400

Asp Thr Gly Asp Tyr Arg Val Tyr Gln Met Pro Ser Phe Leu Gln Ser
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Val Ala Ser Val Leu Leu Tyr Leu Asp Thr Val Pro Glu Val Tyr Thr
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Pro Val Leu Glu His Leu Val Val Met Gln Ile Asp Ser Phe Pro Gln
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Tyr Ser Pro Lys Met Gln Leu Val Cys Cys Arg Ala Ile Val Lys Val
450 455 460

Phe Leu Ala Leu Ala Ala Lys Gly Pro Val Leu Arg Asn Cys Ile Ser
465 470 475 480

Thr Val Val His Gln Gly Leu Ile Arg Ile Cys Ser Lys Pro Val Val
485 490 495

Leu Pro Lys Gly Pro Glu Ser Glu Asp His Arg Ala Ser Gly
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Glu Val Arg Thr Gly Lys Trp Lys Val Pro Thr Tyr Lys Asp Tyr Val
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Asp Leu Phe Arg His Leu Leu Ser Ser Asp Gln Met Met Asp Ser Ile
530 535 540

Leu Ala Asp Glu Ala Phe Phe Ser Val Asn Ser Ser Ser Glu Ser Leu
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Asn His Leu Leu Tyr Asp Glu Phe Val Lys Ser Val Leu Lys Ile Val
565 570 575

Glu Lys Leu Asp Leu Thr Leu Glu Ile Gln Thr Val Gly Glu Gln Glu
580 585 590

Asn Gly Asp Glu Ala Pro Gly Val Trp Met Ile Pro Thr Ser Asp Pro
595 600 605

Ala Ala Asn Leu His Pro Ala Lys Pro Lys Asp Phe Ser Ala Phe Ile
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Asn Leu Val Glu Phe Cys Arg Glu Ile Leu Pro Glu Lys Gln Ala Glu
625 630 635 640

Phe Phe Glu Pro Trp Val Tyr Ser Phe Ser Tyr Glu Leu Ile Leu Gln
645 650 655

Ser Thr Arg Leu Pro Leu Ile Ser Gly Phe Tyr Lys Leu Leu Ser Ile
660 665 670

Thr Val Arg Asn Ala Lys Lys Ile Lys Tyr Phe Glu Gly Val Ser Pro
675 680 685

Lys Ser Leu Lys His Ser Pro Glu Asp Pro Glu Lys Tyr Ser Cys Phe
690 695 700

Ala Leu Phe Val Lys Phe Gly Lys Glu Val Ala Val Lys Met Lys Gln
705 710 715 720

Tyr Lys Asp Glu Leu Leu Ala Ser Cys Leu Thr Phe Leu Leu Ser Leu
725 730 735

Pro His Asn Ile Ile Glu Leu Asp Val Arg Ala Tyr Val Pro Ala Leu
740 745 750

Gln Met Ala Phe Lys Leu Gly Leu Ser Tyr Thr Pro Leu Ala Glu Val
755 760 765

Gly Leu Asn Ala Leu Glu Glu Trp Ser Ile Tyr Ile Asp Arg His Val
770 775 780

Met Gln Pro Tyr Tyr Lys Asp Ile Leu Pro Cys Leu Asp Gly Tyr Leu
785 790 795 800

Lys Thr Ser Ala Leu Ser Asp Glu Thr Lys Asn Asn Trp Glu Val Ser
805 810 815

Ala Leu Ser Arg Ala Ala Gln Lys Gly Phe Asn Lys Val Val Leu Lys
820 825 830

His Leu Lys Lys Thr Lys Asn Leu Ser Ser Asn Glu Ala Ile Ser Leu
835 840 845

Glu Glu Ile Arg Ile Arg Val Val Gln Met Leu Gly Ser Leu Gly Gly
850 855 860

Gln Ile Asn Lys Asn Leu Leu Thr Val Thr Ser Ser Asp Glu Met Met
865 870 875 880

Lys Ser Tyr Val Ala Trp Asp Arg Glu Lys Arg Leu Ser Phe Ala Val
885 890 895

Pro Phe Arg Glu Met Lys Pro Val Ile Phe Leu Asp Val Phe Leu Pro
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Arg Val Thr Glu Leu Ala Leu Thr Ala Ser Asp Arg Gln Thr Lys Val

915

920

925

Ala Ala Cys Glu Leu Leu His Ser Met Val Met Phe Met Leu Gly Lys
930 935 940

Ala Thr Gln Met Pro Glu Gly Gly Gln Gly Ala Pro Pro Met Tyr Gln
945 950 955 960

Leu Tyr Lys Arg Thr Phe Pro Val Leu Leu Arg Leu Ala Cys Asp Val
965 970 975

Asp Gln Val Thr Arg Gln Leu Tyr Glu Pro Leu Val Met Gln Leu Ile
980 985 990

His Trp Phe Thr Asn Asn Lys Lys Phe Glu Ser Gln Asp Thr Val Ser
995 1000 1005

Leu Leu Glu Ala Ile Leu Asp Gly Ile Val Asp Pro Val Asp Ser
1010 1015 1020

Thr Leu Arg Asp Phe Cys Gly Arg Cys Ile Arg Glu Phe Leu Lys
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Trp Ser Ile Lys Gln Ile Thr Pro Gln Gln Glu Lys Ser Pro
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Val Asn Thr Lys Ser Leu Phe Lys Arg Leu Tyr Ser Leu Ala Leu
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His Pro Asn Ala Phe Lys Arg Leu Gly Ala Ser Leu Ala Phe Asn
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Asn Ile Tyr Arg Glu Phe Arg Glu Glu Glu Ser Leu Val Glu Gln
1085 1090 1095

Phe Val Phe Glu Ala Leu Val Ile Tyr Met Glu Ser Leu Ala Leu
1100 1105 1110

Ala His Ala Asp Glu Lys Ser Leu Gly Thr Ile Gln Gln Cys Cys
1115 1120 1125

Asp Ala Ile Asp His Leu Cys Arg Ile Ile Glu Lys Lys His Val
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Ser Leu Asn Lys Ala Lys Lys Arg Arg Leu Pro Arg Gly Phe Pro
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Pro Ser Ala Ser Leu Cys Leu Leu Asp Leu Val Lys Trp Leu Leu
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Ala His Cys Gly Arg Pro Gln Thr Glu Cys Arg His Lys Ser Ile
1175 1180 1185

Glu Leu Phe Tyr Lys Phe Val Pro Leu Leu Pro Gly Asn Arg Ser
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Pro Asn Leu Trp Leu Lys Asp Val Leu Lys Glu Glu Gly Val Ser
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Phe Leu Ile Asn Thr Phe Glu Gly Gly Cys Gly Gln Pro Ser
1220 1225 1230

Gly Ile Leu Ala Gln Pro Thr Leu Leu Tyr Leu Arg Gly Pro Phe
1235 1240 1245

Ser Leu Gln Ala Thr Leu Cys Trp Leu Asp Leu Leu Leu Ala Ala
1250 1255 1260

Leu Glu Cys Tyr Asn Thr Phe Ile Gly Glu Arg Thr Val Gly Ala
1265 1270 1275

Leu Gln Val Leu Gly Thr Glu Ala Gln Ser Ser Leu Leu Lys Ala
1280 1285 1290

Val Ala Phe Phe Leu Glu Ser Ile Ala Met His Asp Ile Ile Ala
1295 1300 1305

Ala Glu Lys Cys Phe Gly Thr Gly Ala Ala Gly Asn Arg Thr Ser
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Pro Gln Glu Gly Glu Arg Tyr Asn Tyr Ser Lys Cys Thr Val Val
1325 1330 1335

Val Arg Ile Met Glu Phe Thr Thr Thr Leu Leu Asn Thr Ser Pro
1340 1345 1350

Glu Gly Trp Lys Leu Leu Lys Lys Asp Leu Cys Asn Thr His Leu
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Met Arg Val Leu Val Gln Thr Leu Cys Glu Pro Ala Ser Ile Gly
1370 1375 1380

Phe Asn Ile Gly Asp Val Gln Val Met Ala His Leu Pro Asp Val
1385 1390 1395

Cys Val Asn Leu Met Lys Ala Leu Lys Met Ser Pro Tyr Lys Asp
1400 1405 1410

Ile Leu Glu Thr His Leu Arg Glu Lys Ile Thr Ala Gln Ser Ile
1415 1420 1425

Glu Glu Leu Cys Ala Val Asn Leu Tyr Gly Pro Asp Ala Gln Val
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Asp Arg Ser Arg Leu Ala Ala Val Val Ser Ala Cys Lys Gln Leu
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His Arg Ala Gly Leu Leu His Asn Ile Leu Pro Ser Gln Ser Thr
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Asp Leu His His Ser Val Gly Thr Glu Leu Leu Ser Leu Val Tyr
1475 1480 1485

Lys Gly Ile Ala Pro Gly Asp Glu Arg Gln Cys Leu Pro Ser Leu
1490 1495 1500

Asp Leu Ser Cys Lys Gln Leu Ala Ser Gly Leu Leu Glu Leu Ala
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Phe Ala Phe Gly Gly Leu Cys Glu Arg Leu Val Ser Leu Leu Leu
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Asn Pro Ala Val Leu Ser Thr Ala Ser Leu Gly Ser Ser Gln Gly
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Ser Val Ile His Phe Ser His Gly Glu Tyr Phe Tyr Ser Leu Phe
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Ser Glu Thr Ile Asn Thr Glu Leu Leu Lys Asn Leu Asp Leu Ala
1565 1570 1575

Val Leu Glu Leu Met Gln Ser Ser Val Asp Asn Thr Lys Met Val
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Ser Ala Val Leu Asn Gly Met Leu Asp Gln Ser Phe Arg Glu Arg
1595 1600 1605

Ala Asn Gln Lys His Gln Gly Leu Lys Leu Ala Thr Thr Ile Leu
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Gln His Trp Lys Lys Cys Asp Ser Trp Trp Ala Lys Asp Ser Pro
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Leu Glu Thr Lys Met Ala Val Leu Ala Leu Leu Ala Lys Ile Leu
1640 1645 1650

Gln Ile Asp Ser Ser Val Ser Phe Asn Thr Ser His Gly Ser Phe
1655 1660 1665

Pro Glu Val Phe Thr Thr Tyr Ile Ser Leu Leu Ala Asp Thr Lys
1670 1675 1680

Leu Asp Leu His Leu Lys Gly Gln Ala Val Thr Leu Leu Pro Phe
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Phe Thr Ser Leu Thr Gly Gly Ser Leu Glu Glu Leu Arg Arg Val
1700 1705 1710

Leu Glu Gln Leu Ile Val Ala His Phe Pro Met Gln Ser Arg Glu
1715 1720 1725

Phe Pro Pro Gly Thr Pro Arg Phe Asn Asn Tyr Val Asp Cys Met
1730 1735 1740

Lys Lys Phe Leu Asp Ala Leu Glu Leu Ser Gln Ser Pro Met Leu
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Leu Glu Leu Met Thr Glu Val Leu Cys Arg Glu Gln Gln His Val
1760 1765 1770

Met Glu Glu Leu Phe Gln Ser Ser Phe Arg Arg Ile Ala Arg Arg
1775 1780 1785

Gly Ser Cys Val Thr Gln Val Gly Leu Leu Glu Ser Val Tyr Glu
1790 1795 1800

Met Phe Arg Lys Asp Asp Pro Arg Leu Ser Phe Thr Arg Gln Ser
1805 1810 1815

Phe Val Asp Arg Ser Leu Leu Thr Leu Leu Trp His Cys Ser Leu
1820 1825 1830

Asp Ala Leu Arg Glu Phe Phe Ser Thr Ile Val Val Asp Ala Ile

1835

1840

1845

Asp Val Leu Lys Ser Arg Phe Thr Lys Leu Asn Glu Ser Thr Phe
1850 1855 1860

Asp Thr Gln Ile Thr Lys Lys Met Gly Tyr Tyr Lys Ile Leu Asp
1865 1870 1875

Val Met Tyr Ser Arg Leu Pro Lys Asp Asp Val His Ala Lys Glu
1880 1885 1890

Ser Lys Ile Asn Gln Val Phe His Gly Ser Cys Ile Thr Glu Gly
1895 1900 1905

Asn Glu Leu Thr Lys Thr Leu Ile Lys Leu Cys Tyr Asp Ala Phe
1910 1915 1920

Thr Glu Asn Met Ala Gly Glu Asn Gln Leu Leu Glu Arg Arg Arg
1925 1930 1935

Leu Tyr His Cys Ala Ala Tyr Asn Cys Ala Ile Ser Val Ile Cys
1940 1945 1950

Cys Val Phe Asn Glu Leu Lys Phe Tyr Gln Gly Phe Leu Phe Ser
1955 1960 1965

Glu Lys Pro Glu Lys Asn Leu Leu Ile Phe Glu Asn Leu Ile Asp
1970 1975 1980

Leu Lys Arg Arg Tyr Asn Phe Pro Val Glu Val Glu Val Pro Met
1985 1990 1995

Glu Arg Lys Lys Lys Tyr Ile Glu Ile Arg Lys Glu Ala Arg Glu
2000 2005 2010

Ala Ala Asn Gly Asp Ser Asp Gly Pro Ser Tyr Met Ser Ser Leu
2015 2020 2025

Ser Tyr Leu Ala Asp Ser Thr Leu Ser Glu Glu Met Ser Gln Phe
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Asp Phe Ser Thr Gly Val Gln Ser Tyr Ser Tyr Ser Ser Gln Asp
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Pro Arg Pro Ala Thr Gly Arg Phe Arg Arg Arg Glu Gln Arg Asp
2060 2065 2070

Pro Thr Val His Asp Asp Val Leu Glu Leu Glu Met Asp Glu Leu
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Asn Arg His Glu Cys Met Ala Pro Leu Thr Ala Leu Val Lys His
2090 2095 2100

Met His Arg Ser Leu Gly Pro Pro Gln Gly Glu Glu Asp Ser Val
2105 2110 2115

Pro Arg Asp Leu Pro Ser Trp Met Lys Phe Leu His Gly Lys Leu
2120 2125 2130

Gly Asn Pro Ile Val Pro Leu Asn Ile Arg Leu Phe Leu Ala Lys
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Leu Val Ile Asn Thr Glu Glu Val Phe Arg Pro Tyr Ala Lys His
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Glu Val Leu Ala Asn Arg Leu Leu Asn Phe Leu Met Lys His Val
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Phe His Pro Lys Arg Ala Val Phe Arg His Asn Leu Glu Ile Ile
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Lys Thr Leu Val Glu Cys Trp Lys Asp Cys Leu Ser Ile Pro Tyr
2240 2245 2250

Arg Leu Ile Phe Glu Lys Phe Ser Gly Lys Asp Pro Asn Ser Lys
2255 2260 2265

Asp Asn Ser Val Gly Ile Gln Leu Leu Gly Ile Val Met Ala Asn
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2330 2335 2340

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2345 2350 2355

Lys Phe Ile Val Cys Leu Asn Lys Val Thr Lys Ser Phe Pro Pro
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Leu Ala Asp Arg Phe Met Asn Ala Val Phe Phe Leu Leu Pro Lys
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Val Glu Leu Arg Glu Leu Leu Asn Pro Val Val Glu Phe Val Ser
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Trp Ile His Asp Asn Tyr Arg Asp Pro Glu Ser Glu Thr Asp Asn
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Ser Pro Asp Tyr Pro Asn Pro Met Phe Glu His Pro Leu Ser Glu
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Cys Glu Phe Gln Glu Tyr Thr Ile Asp Ser Asp Trp Arg Phe Arg
2585 2590 2595

Ser Thr Val Leu Thr Pro Met Phe Val Glu Thr Gln Ala Ser Gln
2600 2605 2610

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Trp Pro Val Ala Gly Gln Ile Arg Ala Thr Gln Gln Gln His Asp
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Phe Thr Leu Thr Gln Thr Ala Asp Gly Arg Ser Ser Phe Asp Trp
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Leu Thr Gly Ser Ser Thr Asp Pro Leu Val Asp His Thr Ser Pro
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Ser Ser Asp Ser Leu Leu Phe Ala His Lys Arg Ser Glu Arg Leu
2675 2680 2685

Gln Arg Ala Pro Leu Lys Ser Val Gly Pro Asp Phe Gly Lys Lys
2690 2695 2700

Arg Leu Gly Leu Pro Gly Asp Glu Val Asp Asn Lys Val Lys Gly
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Ala Ala Gly Arg Thr Asp Leu Leu Arg Leu Arg Arg Arg Phe Met
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Ala Glu Gln Lys Arg Glu Lys Glu Ile Lys Ser Glu Leu Lys Met

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2755

2760

Lys Gln Asp Ala Gln Val Val Leu Tyr Arg Ser Tyr Arg His Gly
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His Leu Ala Glu Trp Lys Ser Leu Glu Tyr Cys Ser Thr Ala Ser
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Glu Leu His Tyr Ser Gln Glu Leu Ser Leu Leu Tyr Leu Leu Gln
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Ser Phe Met Gln Asn Tyr Ser Ser Ile Asp Val Leu Leu His Gln
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Ser Arg Leu Thr Lys Leu Gln Ser Val Gln Ala Leu Thr Glu Ile
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Gln Glu Phe Ile Ser Phe Ile Ser Lys Gln Gly Asn Leu Ser Ser
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Gln Val Pro Leu Lys Arg Leu Leu Asn Thr Trp Thr Asn Arg Tyr
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Pro Asp Ala Lys Met Asp Pro Met Asn Ile Trp Asp Asp Ile Ile
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Thr Asn Arg Cys Phe Phe Leu Ser Lys Ile Glu Glu Lys Leu Thr
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Pro Ser Asp Arg Met Glu Val Gln Glu Gln Glu Glu Asp Ile Ser
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Val Ser Trp Val Gln Ser Tyr Cys Arg Leu Ser His Cys Arg Ser
3275 3280 3285

Arg Ser Gln Gly Cys Ser Glu Gln Val Leu Thr Val Leu Lys Thr
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Val Ser Leu Leu Asp Glu Asn Asn Val Ser Ser Tyr Leu Ser Lys
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Tyr Arg Ile Ile Ala Asn Ala Leu Ser Ser Glu Pro Ala Cys Leu
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Gly Ser Ser Ser Glu Asp Ser Glu Lys Val Ile Ala Gly Leu Tyr
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Thr Lys Glu Ile Ser Ser Val Pro Cys Trp Gln Phe Ile Ser Trp
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Asp Thr Ser Thr Gly His Lys Asn Lys Glu Phe Val Ala Arg Ile
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Ser Asn Asp Val Arg Ala Glu Leu Ala Lys Thr Pro Val Asn Lys
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Asn Met Leu Leu Leu Lys Met Asn Lys Asp Ser Lys Pro Pro Gly

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3670

3675

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Gly Lys Pro Leu Pro Glu Tyr His Val Arg Ile Ala Gly Phe Asp
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Glu Arg Val Thr Val Met Ala Ser Leu Arg Arg Pro Lys Arg Ile
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Gln Val Met Asn Gly Ile Leu Ala Gln Asp Ser Ala Cys Ser Gln
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Arg Ala Leu Gln Leu Arg Thr Tyr Ser Val Val Pro Met Thr Ser
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Leu Ser Asp Pro Arg Ala Pro Pro Cys Glu Tyr Lys Asp Trp Leu
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Thr Lys Met Ser Gly Lys His Asp Val Gly Ala Tyr Met Leu Met
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Tyr Lys Gly Ala Asn Arg Thr Glu Thr Val Thr Ser Phe Arg Lys
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Arg Met Ser Thr Ser Pro Glu Ala Phe Leu Ala Leu Arg Ser His
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Ala Thr Gln Phe Leu Pro Val Pro Glu Leu Met Pro Phe Arg Leu
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Thr Arg Gln Phe Ile Asn Leu Met Leu Pro Met Lys Glu Thr Gly
3965 3970 3975

Leu Met Tyr Ser Ile Met Val His Ala Leu Arg Ala Phe Arg Ser
3980 3985 3990

Asp Pro Gly Leu Leu Thr Asn Thr Met Asp Val Phe Val Lys Glu
3995 4000 4005

Pro Ser Phe Asp Trp Lys Asn Phe Glu Gln Lys Met Leu Lys Lys
4010 4015 4020

Gly Gly Ser Trp Ile Gln Glu Ile Asn Val Ala Glu Lys Asn Trp
4025 4030 4035

Tyr Pro Arg Gln Lys Ile Cys Tyr Ala Lys Arg Lys Leu Ala Gly
4040 4045 4050

Ala Asn Pro Ala Val Ile Thr Cys Asp Glu Leu Leu Leu Gly His
4055 4060 4065

Glu Lys Ala Pro Ala Phe Arg Asp Tyr Val Ala Val Ala Arg Gly
4070 4075 4080

Ser Lys Asp His Asn Ile Arg Ala Gln Glu Pro Glu Ser Gly Leu
4085 4090 4095

Ser Glu Glu Thr Gln Val Lys Cys Leu Met Asp Gln Ala Thr Asp
4100 4105 4110

Pro Asn Ile Leu Gly Arg Thr Trp Glu Gly Trp Glu Pro Trp Met
4115 4120 4125

<210> 4

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<221> PEPTIDE

<222> (1)..(21)

<223> HUMAN GENETIC ORIGIN

<220>

<221> MOD_RES

<222> (11)..(11)

<223> PHOSPHORYLATION at T2609

<400> 4

Ser Thr Val Leu Thr Pro Met Phe Val Glu Thr Gln Ala Ser Gln Gly
1 5 10 15

Thr Leu Gln Thr Arg
20

<210> 5

<211> 29

<212> PRT

<213> Artificial Sequence

<220>

<221> PEPTIDE

<222> (1)..(29)

<223> HUMAN GENETIC ORIGIN

<220>

<221> MOD_RES

<222> (13)..(13)

<223> PHOSPHORYLATION at S2056

<400> 5

Asp Phe Ser Thr Gly Val Gln Ser Tyr Ser Tyr Ser Ser Gln Asp Pro
1 5 10 15

Arg Pro Ala Thr Gly Arg Phe Arg Arg Arg Glu Gln Arg
20 25

<210> 6

<211> 303

<212> PRT

<213> Artificial Sequence

<220>

<221> PEPTIDE

<222> (1)..(303)

<223> HUMAN GENETIC ORIGIN

<220>

<221> MOD_RES

<222> (177)..(177)

<223> PHOSPHORYLATION at S2056

<400> 6

Met Tyr Ser Arg Leu Pro Lys Asp Asp Val His Ala Lys Glu Ser Lys
1 5 10 15

Ile Asn Gln Val Phe His Gly Ser Cys Ile Thr Glu Gly Asn Glu Leu
20 25 30

Thr Lys Thr Leu Ile Lys Leu Cys Tyr Asp Ala Phe Thr Glu Asn Met
35 40 45

Ala Gly Glu Asn Gln Leu Leu Glu Arg Arg Arg Leu Tyr His Cys Ala
50 55 60

Ala Tyr Asn Cys Ala Ile Ser Val Ile Cys Cys Val Phe Asn Glu Leu
65 70 75 80

Lys Phe Tyr Gln Gly Phe Leu Phe Ser Glu Lys Pro Glu Lys Asn Leu
85 90 95

Leu Ile Phe Glu Asn Leu Ile Asp Leu Lys Arg Arg Tyr Asn Phe Pro
100 105 110

Val Glu Val Glu Val Pro Met Glu Arg Lys Lys Tyr Ile Glu Ile
115 120 125

Arg Lys Glu Ala Arg Glu Ala Ala Asn Gly Asp Ser Asp Gly Pro Ser
130 135 140

Tyr Met Ser Ser Leu Ser Tyr Leu Ala Asp Ser Thr Leu Ser Glu Glu
145 150 155 160

Met Ser Gln Phe Asp Phe Ser Thr Gly Val Gln Ser Tyr Ser Tyr Ser
165 170 175

Ser Gln Asp Pro Arg Pro Ala Thr Gly Arg Phe Arg Arg Glu Gln
180 185 190

Arg Asp Pro Thr Val His Asp Asp Val Leu Glu Leu Glu Met Asp Glu
195 200 205

Leu Asn Arg His Glu Cys Met Ala Pro Leu Thr Ala Leu Val Lys His
210 215 220

Met His Arg Ser Leu Gly Pro Pro Gln Gly Glu Glu Asp Ser Val Pro
225 230 235 240

Arg Asp Leu Pro Ser Trp Met Lys Phe Leu His Gly Lys Leu Gly Asn
245 250 255

Pro Ile Val Pro Leu Asn Ile Arg Leu Phe Leu Ala Lys Leu Val Ile
260 265 270

Asn Thr Glu Glu Val Phe Arg Pro Tyr Ala Lys His Trp Leu Ser Pro
275 280 285

Leu Leu Gln Leu Ala Ala Ser Glu Asn Asn Gly Gly Glu Gly Ile
290 295 300

<210> 7

<211> 388

<212> PRT

<213> Artificial Sequence

<220>

<221> PEPTIDE

<222> (1)..(388)

<223> HUMAN GENETIC ORIGIN

<220>

<221> MOD_RES

<222> (177)..(177)

<223> PHOSPHORYLATION at S2056

<400> 7

Met Tyr Ser Arg Leu Pro Lys Asp Asp Val His Ala Lys Glu Ser Lys
1 5 10 15

Ile Asn Gln Val Phe His Gly Ser Cys Ile Thr Glu Gly Asn Glu Leu
20 25 30

Thr Lys Thr Leu Ile Lys Leu Cys Tyr Asp Ala Phe Thr Glu Asn Met
35 40 45

Ala Gly Glu Asn Gln Leu Leu Glu Arg Arg Arg Leu Tyr His Cys Ala
50 55 60

Ala Tyr Asn Cys Ala Ile Ser Val Ile Cys Cys Val Phe Asn Glu Leu
65 70 75 80

Lys Phe Tyr Gln Gly Phe Leu Phe Ser Glu Lys Pro Glu Lys Asn Leu
85 90 95

Leu Ile Phe Glu Asn Leu Ile Asp Leu Lys Arg Arg Tyr Asn Phe Pro
100 105 110

Val Glu Val Glu Val Pro Met Glu Arg Lys Lys Tyr Ile Glu Ile
115 120 125

Arg Lys Glu Ala Arg Glu Ala Ala Asn Gly Asp Ser Asp Gly Pro Ser
130 135 140

Tyr Met Ser Ser Leu Ser Tyr Leu Ala Asp Ser Thr Leu Ser Glu Glu
145 150 155 160

Met Ser Gln Phe Asp Phe Ser Thr Gly Val Gln Ser Tyr Ser Tyr Ser
165 170 175

Ser Gln Asp Pro Arg Pro Ala Thr Gly Arg Phe Arg Arg Glu Gln
180 185 190

Arg Asp Pro Thr Val His Asp Asp Val Leu Glu Leu Glu Met Asp Glu
195 200 205

Leu Asn Arg His Glu Cys Met Ala Pro Leu Thr Ala Leu Val Lys His
210 215 220

Met His Arg Ser Leu Gly Pro Pro Gln Gly Glu Glu Asp Ser Val Pro
225 230 235 240

Arg Asp Leu Pro Ser Trp Met Lys Phe Leu His Gly Lys Leu Gly Asn
245 250 255

Pro Ile Val Pro Leu Asn Ile Arg Leu Phe Leu Ala Lys Leu Val Ile
260 265 270

Asn Thr Glu Glu Val Phe Arg Pro Tyr Ala Lys His Trp Leu Ser Pro
275 280 285

Leu Leu Gln Leu Ala Ala Ser Glu Asn Asn Gly Gly Glu Gly Ile His
290 295 300

Tyr Met Val Val Glu Ile Val Ala Thr Ile Leu Ser Trp Thr Gly Leu
305 310 315 320

Ala Thr Pro Thr Gly Val Pro Lys Asp Glu Val Leu Ala Asn Arg Leu
325 330 335

Leu Asn Phe Leu Met Lys His Val Phe His Pro Lys Arg Ala Val Phe
340 345 350

Arg His Asn Leu Glu Ile Ile Lys Thr Leu Val Glu Cys Trp Lys Asp
355 360 365

Cys Leu Ser Ile Pro Tyr Arg Leu Ile Phe Glu Lys Phe Ser Gly Lys
370 375 380

Asp Pro Asn Ser
385

<210> 8

<211> 821

<212> PRT

<213> Artificial Sequence

<220>

<221> PEPTIDE

<222> (1)..(821)

<223> HUMAN GENETIC ORIGIN

<220>

<221> MOD_RES

<222> (177)..(177)

<223> PHOSPHORYLATION at S2056

<220>

<221> MOD_RES

<222> (730)..(730)

<223> PHOSPHORYLATION at T2609

<400> 8

Met Tyr Ser Arg Leu Pro Lys Asp Asp Val His Ala Lys Glu Ser Lys
1 5 10 15

Ile Asn Gln Val Phe His Gly Ser Cys Ile Thr Glu Gly Asn Glu Leu
20 25 30

Thr Lys Thr Leu Ile Lys Leu Cys Tyr Asp Ala Phe Thr Glu Asn Met
35 40 45

Ala Gly Glu Asn Gln Leu Leu Glu Arg Arg Arg Leu Tyr His Cys Ala
50 55 60

Ala Tyr Asn Cys Ala Ile Ser Val Ile Cys Cys Val Phe Asn Glu Leu

65

70

75

80

Lys Phe Tyr Gln Gly Phe Leu Phe Ser Glu Lys Pro Glu Lys Asn Leu
85 90 95

Leu Ile Phe Glu Asn Leu Ile Asp Leu Lys Arg Arg Tyr Asn Phe Pro
100 105 110

Val Glu Val Glu Val Pro Met Glu Arg Lys Lys Tyr Ile Glu Ile
115 120 125

Arg Lys Glu Ala Arg Glu Ala Ala Asn Gly Asp Ser Asp Gly Pro Ser
130 135 140

Tyr Met Ser Ser Leu Ser Tyr Leu Ala Asp Ser Thr Leu Ser Glu Glu
145 150 155 160

Met Ser Gln Phe Asp Phe Ser Thr Gly Val Gln Ser Tyr Ser Tyr Ser
165 170 175

Ser Gln Asp Pro Arg Pro Ala Thr Gly Arg Phe Arg Arg Glu Gln
180 185 190

Arg Asp Pro Thr Val His Asp Asp Val Leu Glu Leu Glu Met Asp Glu
195 200 205

Leu Asn Arg His Glu Cys Met Ala Pro Leu Thr Ala Leu Val Lys His
210 215 220

Met His Arg Ser Leu Gly Pro Pro Gln Gly Glu Glu Asp Ser Val Pro
225 230 235 240

Arg Asp Leu Pro Ser Trp Met Lys Phe Leu His Gly Lys Leu Gly Asn
245 250 255

Pro Ile Val Pro Leu Asn Ile Arg Leu Phe Leu Ala Lys Leu Val Ile
260 265 270

Asn Thr Glu Glu Val Phe Arg Pro Tyr Ala Lys His Trp Leu Ser Pro
275 280 285

Leu Leu Gln Leu Ala Ala Ser Glu Asn Asn Gly Gly Glu Gly Ile His
290 295 300

Tyr Met Val Val Glu Ile Val Ala Thr Ile Leu Ser Trp Thr Gly Leu
305 310 315 320

Ala Thr Pro Thr Gly Val Pro Lys Asp Glu Val Leu Ala Asn Arg Leu
325 330 335

Leu Asn Phe Leu Met Lys His Val Phe His Pro Lys Arg Ala Val Phe
340 345 350

Arg His Asn Leu Glu Ile Ile Lys Thr Leu Val Glu Cys Trp Lys Asp
355 360 365

Cys Leu Ser Ile Pro Tyr Arg Leu Ile Phe Glu Lys Phe Ser Gly Lys
370 375 380

Asp Pro Asn Ser Lys Asp Asn Ser Val Gly Ile Gln Leu Leu Gly Ile
385 390 395 400

Val Met Ala Asn Asp Leu Pro Pro Tyr Asp Pro Gln Cys Gly Ile Gln
405 410 415

Ser Ser Glu Tyr Phe Gln Ala Leu Val Asn Asn Met Ser Phe Val Arg
420 425 430

Tyr Lys Glu Val Tyr Ala Ala Ala Glu Val Leu Gly Leu Ile Leu
435 440 445

Arg Tyr Val Met Glu Arg Lys Asn Ile Leu Glu Ser Leu Cys Glu
450 455 460

Leu Val Ala Lys Gln Leu Lys Gln His Gln Asn Thr Met Glu Asp Lys
465 470 475 480

Phe Ile Val Cys Leu Asn Lys Val Thr Lys Ser Phe Pro Pro Leu Ala
485 490 495

Asp Arg Phe Met Asn Ala Val Phe Phe Leu Leu Pro Lys Phe His Gly
500 505 510

Val Leu Lys Thr Leu Cys Leu Glu Val Val Leu Cys Arg Val Glu Gly
515 520 525

Met Thr Glu Leu Tyr Phe Gln Leu Lys Ser Lys Asp Phe Val Gln Val
530 535 540

Met Arg His Arg Asp Asp Glu Arg Gln Lys Val Cys Leu Asp Ile Ile
545 550 555 560

Tyr Lys Met Met Pro Lys Leu Lys Pro Val Glu Leu Arg Glu Leu Leu
565 570 575

Asn Pro Val Val Glu Phe Val Ser His Pro Ser Thr Thr Cys Arg Glu
580 585 590

Gln Met Tyr Asn Ile Leu Met Trp Ile His Asp Asn Tyr Arg Asp Pro
595 600 605

Glu Ser Glu Thr Asp Asn Asp Ser Gln Glu Ile Phe Lys Leu Ala Lys
610 615 620

Asp Val Leu Ile Gln Gly Leu Ile Asp Glu Asn Pro Gly Leu Gln Leu
625 630 640

Ile Ile Arg Asn Phe Trp Ser His Glu Thr Arg Leu Pro Ser Asn Thr
645 650 655

Leu Asp Arg Leu Leu Ala Leu Asn Ser Leu Tyr Ser Pro Lys Ile Glu
660 665 670

Val His Phe Leu Ser Leu Ala Thr Asn Phe Leu Leu Glu Met Thr Ser
675 680 685

Met Ser Pro Asp Tyr Pro Asn Pro Met Phe Glu His Pro Leu Ser Glu
690 695 700

Cys Glu Phe Gln Glu Tyr Thr Ile Asp Ser Asp Trp Arg Phe Arg Ser
705 710 715 720

Thr Val Leu Thr Pro Met Phe Val Glu Thr Gln Ala Ser Gln Gly Thr
725 730 735

Leu Gln Thr Arg Thr Gln Glu Gly Ser Leu Ser Ala Arg Trp Pro Val
740 745 750

Ala Gly Gln Ile Arg Ala Thr Gln Gln Gln His Asp Phe Thr Leu Thr
755 760 765

Gln Thr Ala Asp Gly Arg Ser Ser Phe Asp Trp Leu Thr Gly Ser Ser
770 775 780

Thr Asp Pro Leu Val Asp His Thr Ser Pro Ser Ser Asp Ser Leu Leu
785 790 795 800

Phe Ala His Lys Arg Ser Glu Arg Leu Gln Arg Ala Pro Leu Lys Ser
805 810 815

Val Gly Pro Asp Phe
820

<210> 9

<211> 440

<212> PRT

<213> Artificial Sequence

<220>

<221> PEPTIDE

<222> (1)..(440)

<223> HUMAN GENETIC ORIGIN

<220>

<221> MOD_RES

<222> (349)..(349)

<223> PHOSPHORYLATION at T2609

<400> 9

Ser Gly Lys Asp Pro Asn Ser Lys Asp Asn Ser Val Gly Ile Gln Leu
1 5 10 15

Leu Gly Ile Val Met Ala Asn Asp Leu Pro Pro Tyr Asp Pro Gln Cys
20 25 30

Gly Ile Gln Ser Ser Glu Tyr Phe Gln Ala Leu Val Asn Asn Met Ser
35 40 45

Phe Val Arg Tyr Lys Glu Val Tyr Ala Ala Ala Ala Glu Val Leu Gly
50 55 60

Leu Ile Leu Arg Tyr Val Met Glu Arg Lys Asn Ile Leu Glu Glu Ser
65 70 75 80

Leu Cys Glu Leu Val Ala Lys Gln Leu Lys Gln His Gln Asn Thr Met
85 90 95

Glu Asp Lys Phe Ile Val Cys Leu Asn Lys Val Thr Lys Ser Phe Pro
100 105 110

Pro Leu Ala Asp Arg Phe Met Asn Ala Val Phe Phe Leu Leu Pro Lys
115 120 125

Phe His Gly Val Leu Lys Thr Leu Cys Leu Glu Val Val Leu Cys Arg
130 135 140

Val Glu Gly Met Thr Glu Leu Tyr Phe Gln Leu Lys Ser Lys Asp Phe
145 150 155 160

Val Gln Val Met Arg His Arg Asp Asp Glu Arg Gln Lys Val Cys Leu
165 170 175

Asp Ile Ile Tyr Lys Met Met Pro Lys Leu Lys Pro Val Glu Leu Arg
180 185 190

Glu Leu Leu Asn Pro Val Val Glu Phe Val Ser His Pro Ser Thr Thr
195 200 205

Cys Arg Glu Gln Met Tyr Asn Ile Leu Met Trp Ile His Asp Asn Tyr
210 215 220

Arg Asp Pro Glu Ser Glu Thr Asp Asn Asp Ser Gln Glu Ile Phe Lys
225 230 235 240

Leu Ala Lys Asp Val Leu Ile Gln Gly Leu Ile Asp Glu Asn Pro Gly
245 250 255

Leu Gln Leu Ile Ile Arg Asn Phe Trp Ser His Glu Thr Arg Leu Pro
260 265 270

Ser Asn Thr Leu Asp Arg Leu Leu Ala Leu Asn Ser Leu Tyr Ser Pro
275 280 285

Lys Ile Glu Val His Phe Leu Ser Leu Ala Thr Asn Phe Leu Leu Glu
290 295 300

Met Thr Ser Met Ser Pro Asp Tyr Pro Asn Pro Met Phe Glu His Pro
305 310 315 320

Leu Ser Glu Cys Glu Phe Gln Glu Tyr Thr Ile Asp Ser Asp Trp Arg
325 330 335

Phe Arg Ser Thr Val Leu Thr Pro Met Phe Val Glu Thr Gln Ala Ser
340 345 350

Gln Gly Thr Leu Gln Thr Arg Thr Gln Glu Gly Ser Leu Ser Ala Arg
355 360 365

Trp Pro Val Ala Gly Gln Ile Arg Ala Thr Gln Gln Gln His Asp Phe
370 375 380

Thr Leu Thr Gln Thr Ala Asp Gly Arg Ser Ser Phe Asp Trp Leu Thr
385 390 395 400

Gly Ser Ser Thr Asp Pro Leu Val Asp His Thr Ser Pro Ser Ser Asp
405 410 415

Ser Leu Leu Phe Ala His Lys Arg Ser Glu Arg Leu Gln Arg Ala Pro
420 425 430

Leu Lys Ser Val Gly Pro Asp Phe
435 440

<210> 10
<211> 200
<212> PRT
<213> Artificial Sequence

<220>
<221> PEPTIDE
<222> (1)..(200)
<223> HUMAN GENETIC ORIGIN

<220>
<221> MOD_RES
<222> (109)..(109)
<223> PHOSPHORYLATION at T2609

<400> 10

Leu Ala Lys Asp Val Leu Ile Gln Gly Leu Ile Asp Glu Asn Pro Gly
1 5 10 15

Leu Gln Leu Ile Ile Arg Asn Phe Trp Ser His Glu Thr Arg Leu Pro
20 25 30

Ser Asn Thr Leu Asp Arg Leu Leu Ala Leu Asn Ser Leu Tyr Ser Pro
35 40 45

Lys Ile Glu Val His Phe Leu Ser Leu Ala Thr Asn Phe Leu Leu Glu
50 55 60

Met Thr Ser Met Ser Pro Asp Tyr Pro Asn Pro Met Phe Glu His Pro
65 70 75 80

Leu Ser Glu Cys Glu Phe Gln Glu Tyr Thr Ile Asp Ser Asp Trp Arg
85 90 95

Phe Arg Ser Thr Val Leu Thr Pro Met Phe Val Glu Thr Gln Ala Ser
100 105 110

Gln Gly Thr Leu Gln Thr Arg Thr Gln Glu Gly Ser Leu Ser Ala Arg
115 120 125

Trp Pro Val Ala Gly Gln Ile Arg Ala Thr Gln Gln Gln His Asp Phe
130 135 140

Thr Leu Thr Gln Thr Ala Asp Gly Arg Ser Ser Phe Asp Trp Leu Thr
145 150 155 160

Gly Ser Ser Thr Asp Pro Leu Val Asp His Thr Ser Pro Ser Ser Asp
165 170 175

Ser Leu Leu Phe Ala His Lys Arg Ser Glu Arg Leu Gln Arg Ala Pro
180 185 190

Leu Lys Ser Val Gly Pro Asp Phe
195 200

<210> 11

<211> 428

<212> PRT

<213> Artificial Sequence

<220>

<221> PEPTIDE

<222> (1)...(428)

<223> HUMAN GENETIC ORIGIN

<220>

<221> MOD_RES

<222> (335)...(335)

<223> PHOSPHORYLATION at T2609

<400> 11

Gln Leu Leu Gly Ile Val Met Ala Asn Asp Leu Pro Pro Tyr Asp Pro
1 5 10 15

Gln Cys Gly Ile Gln Ser Ser Glu Tyr Phe Gln Ala Leu Val Asn Asn
20 25 30

Met Ser Phe Val Arg Tyr Lys Glu Val Tyr Ala Ala Ala Glu Val
35 40 45

Leu Gly Leu Ile Leu Arg Tyr Val Met Glu Arg Lys Asn Ile Leu Glu
50 55 60

Glu Ser Leu Cys Glu Leu Val Ala Lys Gln Leu Lys Gln His Gln Asn
65 70 75 80

Thr Met Glu Asp Lys Phe Ile Val Cys Leu Asn Lys Val Thr Lys Ser
85 90 95

Phe Pro Pro Leu Ala Asp Arg Phe Met Asn Ala Val Phe Phe Leu Leu
100 105 110

Pro Lys Phe His Gly Val Leu Lys Thr Leu Cys Leu Glu Val Val Leu
115 120 125

Cys Arg Val Glu Gly Met Thr Glu Leu Tyr Phe Gln Leu Lys Ser Lys
130 135 140

Asp Phe Val Gln Val Met Arg His Arg Asp Asp Glu Arg Gln Lys Val
145 150 155 160

Cys Leu Asp Ile Ile Tyr Lys Met Met Pro Lys Leu Lys Pro Val Glu
165 170 175

Leu Arg Glu Leu Leu Asn Pro Val Val Glu Phe Val Ser His Pro Ser
180 185 190

Thr Thr Cys Arg Glu Gln Met Tyr Asn Ile Leu Met Trp Ile His Asp
195 200 205

Asn Tyr Arg Asp Pro Glu Ser Glu Thr Asp Asn Asp Ser Gln Glu Ile
210 215 220

Phe Lys Leu Ala Lys Asp Val Leu Ile Gln Gly Leu Ile Asp Glu Asn
225 230 235 240

Pro Gly Leu Gln Leu Ile Ile Arg Asn Phe Trp Ser His Glu Thr Arg
245 250 255

Leu Pro Ser Asn Thr Leu Asp Arg Leu Leu Ala Leu Asn Ser Leu Tyr
260 265 270

Ser Pro Lys Ile Glu Val His Phe Leu Ser Leu Ala Thr Asn Phe Leu
275 280 285

Leu Glu Met Thr Ser Met Ser Pro Asp Tyr Pro Asn Pro Met Phe Glu
290 295 300

His Pro Leu Ser Glu Cys Glu Phe Gln Glu Tyr Thr Ile Asp Ser Asp
305 310 315 320

Trp Arg Phe Arg Ser Thr Val Leu Thr Pro Met Phe Val Glu Thr Gln
325 330 335

Ala Ser Gln Gly Thr Leu Gln Thr Arg Thr Gln Glu Gly Ser Leu Ser
340 345 350

Ala Arg Trp Pro Val Ala Gly Gln Ile Arg Ala Thr Gln Gln Gln His
355 360 365

Asp Phe Thr Leu Thr Gln Thr Ala Asp Gly Arg Ser Ser Phe Asp Trp
370 375 380

Leu Thr Gly Ser Ser Thr Asp Pro Leu Val Asp His Thr Ser Pro Ser
385 390 395 400

Ser Asp Ser Leu Leu Phe Ala His Lys Arg Ser Glu Arg Leu Gln Arg
405 410 415

Ala Pro Leu Lys Ser Val Gly Pro Asp Phe Gly Lys
420 425

<210> 12

<211> 273

<212> PRT

<213> Artificial Sequence

<220>

<221> PEPTIDE

<222> (1)..(273)

<223> HUMAN GENETIC ORIGIN

<220>

<221> MOD_RES

<222> (180)..(180)

<223> PHOSPHORYLATION at T2609

<400> 12

Glu Arg Gln Lys Val Cys Leu Asp Ile Ile Tyr Lys Met Met Pro Lys
1 5 10 15

Leu Lys Pro Val Glu Leu Arg Glu Leu Leu Asn Pro Val Val Glu Phe
20 25 30

Val Ser His Pro Ser Thr Thr Cys Arg Glu Gln Met Tyr Asn Ile Leu
35 40 45

Met Trp Ile His Asp Asn Tyr Arg Asp Pro Glu Ser Glu Thr Asp Asn
50 55 60

Asp Ser Gln Glu Ile Phe Lys Leu Ala Lys Asp Val Leu Ile Gln Gly
65 70 75 80

Leu Ile Asp Glu Asn Pro Gly Leu Gln Leu Ile Ile Arg Asn Phe Trp
85 90 95

Ser His Glu Thr Arg Leu Pro Ser Asn Thr Leu Asp Arg Leu Leu Ala
100 105 110

Leu Asn Ser Leu Tyr Ser Pro Lys Ile Glu Val His Phe Leu Ser Leu
115 120 125

Ala Thr Asn Phe Leu Leu Glu Met Thr Ser Met Ser Pro Asp Tyr Pro
130 135 140

Asn Pro Met Phe Glu His Pro Leu Ser Glu Cys Glu Phe Gln Glu Tyr
145 150 155 160

Thr Ile Asp Ser Asp Trp Arg Phe Arg Ser Thr Val Leu Thr Pro Met
165 170 175

Phe Val Glu Thr Gln Ala Ser Gln Gly Thr Leu Gln Thr Arg Thr Gln
180 185 190

Glu Gly Ser Leu Ser Ala Arg Trp Pro Val Ala Gly Gln Ile Arg Ala
195 200 205

Thr Gln Gln Gln His Asp Phe Thr Leu Thr Gln Thr Ala Asp Gly Arg
210 215 220

Ser Ser Phe Asp Trp Leu Thr Gly Ser Ser Thr Asp Pro Leu Val Asp
225 230 235 240

His Thr Ser Pro Ser Ser Asp Ser Leu Leu Phe Ala His Lys Arg Ser
245 250 255

Glu Arg Leu Gln Arg Ala Pro Leu Lys Ser Val Gly Pro Asp Phe Gly
260 265 270

Lys

<210> 13

<211> 140

<212> PRT
<213> Artificial Sequence

<220>
<221> PEPTIDE
<222> (1)...(140)
<223> HUMAN GENETIC ORIGIN

<220>
<221> MOD_RES
<222> (49)...(49)
<223> PHOSPHORYLATION at T2609

<400> 13

Phe Leu Leu Glu Met Thr Ser Met Ser Pro Asp Tyr Pro Asn Pro Met
1 5 10 15

Phe Glu His Pro Leu Ser Glu Cys Glu Phe Gln Glu Tyr Thr Ile Asp
20 25 30

Ser Asp Trp Arg Phe Arg Ser Thr Val Leu Thr Pro Met Phe Val Glu
35 40 45

Thr Gln Ala Ser Gln Gly Thr Leu Gln Thr Arg Thr Gln Glu Gly Ser
50 55 60

Leu Ser Ala Arg Trp Pro Val Ala Gly Gln Ile Arg Ala Thr Gln Gln
65 70 75 80

Gln His Asp Phe Thr Leu Thr Gln Thr Ala Asp Gly Arg Ser Ser Phe
85 90 95

Asp Trp Leu Thr Gly Ser Ser Thr Asp Pro Leu Val Asp His Thr Ser
100 105 110

Pro Ser Ser Asp Ser Leu Leu Phe Ala His Lys Arg Ser Glu Arg Leu
115 120 125

Gln Arg Ala Pro Leu Lys Ser Val Gly Pro Asp Phe
130 135 140

<210> 14

<211> 102
<212> PRT
<213> Artificial Sequence

<220>
<221> PEPTIDE
<222> (1)...(102)
<223> HUMAN GENETIC ORIGIN

<220>
<221> MOD_RES
<222> (9)..(9)
<223> PHOSPHORYLATION at T2609

<400> 14

Val Leu Thr Pro Met Phe Val Glu Thr Gln Ala Ser Gln Gly Thr Leu
1 5 10 15

Gln Thr Arg Thr Gln Glu Gly Ser Leu Ser Ala Arg Trp Pro Val Ala
20 25 30

Gly Gln Ile Arg Ala Thr Gln Gln Gln His Asp Phe Thr Leu Thr Gln
35 40 45

Thr Ala Asp Gly Arg Ser Ser Phe Asp Trp Leu Thr Gly Ser Ser Thr
50 55 60

Asp Pro Leu Val Asp His Thr Ser Pro Ser Ser Asp Ser Leu Leu Phe
65 70 75 80

Ala His Lys Arg Ser Glu Arg Leu Gln Arg Ala Pro Leu Lys Ser Val
85 90 95

Gly Pro Asp Phe Gly Lys
100

<210> 15

<211> 13509

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (6233)..(6235)

<223> Encodes S2056

<220>

<221> misc_feature

<222> (7882)..(7884)

<223> Encodes T2609

<400> 15

ggggcatttc cgggtccggg ccgagcgggc gcacgcggg gagcgggact cggcggcatg 60

gcgggctccg gagccggtgt gcgttgctcc ctgctgcggc tgcaggagac cttgtccgct 120

gcggaccgct gcgggtctgc cctggccggt catcaactga tccgcggcct ggggcaggaa 180

tgcgtcctga gcagcagccc cgccgtgctg gcattacaga catcttttagt tttttccaga 240

gattcggtt tgcttgatt tgtccggaag tcactcaaca gtattgaatt tcgtgaatgt 300
agagaagaaa tcctaaagtt tttatgtatt ttcttagaaa aatgggcca gaagatcgca 360
ccttactctg ttgaaattaa gaacacttgtt accagtgtt atacaaaaga tagagctgct 420
aaatgtaaaa ttccagccct ggaccttctt attaagttac ttcaagactt tagaagttct 480
agactcatgg atgaattaa aattggagaa ttatttagta aattctatgg agaacttgca 540
ttgaaaaaaaaa aaataccaga tacagttta gaaaaagtat atgagctcct aggattattg 600
ggtgaagttc atcctagtga gatgataaat aatgcagaaa acctgttccg cgctttctg 660
ggtaactta agacccagat gacatcagca gtaagagagc ccaaactacc tgttctggca 720
ggatgtctga aggggttgc ctcacttctg tgcaacttca ctaagtccat ggaagaagat 780
ccccagactt caagggagat tttaatttt gtactaaagg caattcgtcc tcagattgat 840
ctgaagagat atgctgtgcc ctcagctggc ttgcgcctat ttgcgcctgca tgcatctcag 900
tttagcacct gccttctgga caactacgtg tctctattt aagtcttgtt aaagtgggt 960
gcccacacaa atgtagaatt gaaaaagct gcactttcag ccctggaatc ctttctgaaa 1020
caggttcta atatggggc gaaaaatgca gaaatgcata aaaataaact gcagttacttt 1080
atggagcagt tttatggaat catcagaaat gtggattcga acaacaagga gttatctatt 1140
gctatccgtg gatatggact tttgcagga ccgtcaagg ttataaacgc aaaagatgtt 1200
gacttcatgt acgttgagct cattcagcgc tgcaagcaga tgccctcac ccagacagac 1260
actggtgacg accgtgttta tcagatgcc a gcttcctcc agtctgtgc a a g c g t c t t g 1320
ctgtacctt acacagttcc tgaggtgtat actccagttc tggagcacct cgtggtgatg 1380
cagatagaca gtttcccaca gtacagtcca aaaatgcagc tgggtgttg cagagccata 1440
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tacgcgaagc actggcttag ccccttgctg cagctggctg cttctgaaaa caatggagga 900
gaaggaatt 909

<210> 19
 <211> 1164
 <212> DNA
 <213> Artificial sequence
 <220>
 <223> Cloned DNA sequence encoding the 1879-2267 peptide
 <220>
 <221> CDS
 <222> (1)..(1164)
 <223> HUMAN GENETIC ORIGIN
 <220>
 <221> misc_feature
 <222> (529)..(531)
 <223> encodes S2056 residue
 <400> 19

atgtattctc gccttccaa agatgatgtt catgctaagg aatcaaaaat taatcaagtt	60
ttccatggct cgtgttattac agaaggaaat gaacttacaa agacattgat taaattgtgc	120
tacgatgcat ttacagagaa catggcagga gagaatcagc tgctggagag gagaagactt	180
taccattgtg cagcatacaa ctgcgccata tctgtcatct gctgtgtctt caatgagttt	240
aaattttacc aaggtttct gtttagtgaa aaaccagaaa agaacttgc tattttgaa	300
aatctgatcg acctgaagcg ccgctataat tttcctgttag aagttgaggt tcctatggaa	360
agaaagaaaa agtacattga aatttagggaa gaagccagag aagcagcaaa tggggattca	420
gatggtcctt cctatatgtc ttccctgtca tatttggcag acagtaccct gagtgaggaa	480
atgagtcaat ttgatttctc aaccggagtt cagagctatt catacagctc ccaagaccct	540
agacctgcca ctggtcgttt tcggagacgg gagcagcggg accccacggt gcatgatgat	600
gtgctggagc tggagatgga cgagctaat cggcatgagt gcatggcgcc cctgacggcc	660
ctggtaagc acatgcacag aagcctgggc ccgcctcaag gagaagagga ttcaagtgc	720
agagatcttc cttcttggat gaaattcctc catggcaaac tggaaatcc aatagttacca	780
ttaaatatcc gtctttctt agccaagctt gttattaata cagaagaggt ctccgcctt	840
tacgcgaagc actggcttag ccccttgctg cagctggctg cttctgaaaa caatggagga	900
gaaggaattc actacatggt ggtttagata gtggccacta ttcttcatg gacaggctt	960
gccactccaa caggggtccc taaagatgaa gtgttagcaa atcgattgct taatttccta	1020
atgaaacatg tctttcatcc aaaaagagct gtgttagac acaaccttga aattataaag	1080
acccttgcg agtgctggaa ggattgttta tccatccctt ataggttaat atttgaaaag	1140

tttccggta aagatcctaa ttct

1164

<210> 20

<211> 2463

<212> DNA

<213> Artificial Sequence

<220>

<223> cDNA sequence encoding the 1879-2700 peptide

<220>

<221> CDS

<222> (1)..(2463)

<223> HUMAN GENETIC ORIGIN

<220>

<221> misc_feature

<222> (529)..(531)

<223> encodes S2056 residue

<220>

<221> misc_feature

<222> (2188)..(2190)

<223> encodes T2609 residue

<400> 20

atgtattctc gccttccaa agatgtatgtt catgctaagg aatcaaaaat taatcaagtt 60

ttccatggct cgtgttattac agaaggaaat gaacttacaa agacattgtat taaattgtgc 120

tacgatgcat ttacagagaa catggcagga gagaatcagc tgctggagag gagaagactt 180

taccattgtg cagcatacaa ctgcgccata tctgtcatct gctgtgtctt caatgagttt 240

aaattttacc aaggttttct gtttagtgaa aaaccagaaa agaacttgc tattttgaa 300

aatctgatcg acctgaagcg ccgctataat tttcctgttag aagttgaggt tcctatggaa 360

agaaagaaaa agtacattga aatttaggaaa gaagccagag aagcagcaaa tgggattca 420

gatggtcctt cctatatgtc ttccctgtca tatttggcag acagtaccct gagtgaggaa 480

atgagtcaat ttgatttctc aaccggagtt cagacttatt catacagctc ccaagaccct 540

agacctgcca ctggtcgttt tcggagacgg gagcagcggg accccacggt gcatgatgat 600

gtgctggagc tggagatgga cgagctaat cggcatgagt gcatggcgcc cctgacggcc 660

ctggtaagc acatgcacag aagcctgggc ccgcctcaag gagaagagga ttcaagtgc 720

agagatcttc cttcttggat gaaattcctc catggcaaac tggaaatcc aatagtagcca 780

ttaaatatcc gtctttctt agccaagctt gttattaata cagaagaggt ctccgcctt 840

tacgcgaagc actggcttag ccccttgctg cagctggctg cttctgaaaa caatggagga 900

gaaggaattc actacatggt ggtttagata gtggccacta ttctttcatg gacaggctt 960

gccactccaa caggggtccc taaagatgaa gtgttagcaa atcgattgct taatcccta	1020
atgaaacatg tcttcatcc aaaaagagct gtgttagac acaaccttga aattataaag	1080
acccttgcg agtgcgtgaa ggattgtta tccatccctt ataggttaat attgaaaag	1140
ttttccggta aagatcctaa ttctaaagac aactcagtag ggattcaatt gctaggcatc	1200
gtgatggcca atgacctgcc tccctatgac ccacagtgtg gcatccagag tagcgaatac	1260
ttccaggctt tggtaataa tatgtcctt gtaagatata aagaagtgt a tgccgctgca	1320
gcagaagttc taggacttat acttcgatat gttatggaga gaaaaaact actggaggag	1380
tctctgtgtg aactgggtgc gaaacaattt aagcaacatc agaatactat ggaggacaag	1440
tttattgtgt gcttgaacaa agtgaccaag agcttccctc ctcttgcaga caggttcatg	1500
aatgctgtgt tcttcgtct gccaaaattt catggagtgt tgaaaacact ctgtctggag	1560
gtggtaactt gtcgtgtgaa gggaaatgaca gagctgtact tccagttaa gagcaaggac	1620
ttcggtcaag tcatgagaca tagagatgat gaaagacaaa aagtatgttt ggacataatt	1680
tataagatga tgccaaagtt aaaaccagta gaactccgag aacttctgaa ccccggtgt	1740
gaattcggtt cccatccttc tacaacatgt agggaaacaaa tgtataatat tctcatgtgg	1800
attcatgata attacagaga tccagaaagt gagacagata atgactccca gggaaatattt	1860
aagttggcaa aagatgtgct gattcaagga ttgatcgatg agaaccctgg acttcaatta	1920
attattcgaa atttctggag ccatgaaact aggttacctt caaatacctt ggaccgggt	1980
ctggcactaa attccttata ttctcctaag atagaagtgc acttttaag ttttagcaaca	2040
aattttctgc tcgaaatgac cagcatgagc ccagattatc caaaccctt gttcgagcat	2100
cctctgtcag aatgcgaatt tcaggaatat accattgatt ctgattggcg tttccgaagt	2160
actgttctca ctccgatgtt tgtggagacc caggcctccc agggcactct ccagaccgt	2220
accaggaaag ggtccctctc agctcgctgg ccagtggcag ggcagataag ggccacccag	2280
cagcagcatg acttcacact gacacagact gcagatggaa gaagctcatt tgattggctg	2340
accgggagca gcactgaccc gctggtcgac cacaccagtc cctcatctga ctccttgctg	2400
tttggccaca agaggagtga aaggttacag agagcaccct tgaagtcaat gggccctgat	2460
ttt	2463

<210> 21

<211> 1320

<212> DNA

<213> Artificial sequence

<220>

<223> cDNA sequence encoding the 2261-2700 peptide

<220>

<221> CDS

<222> (1)..(1320)

<223> HUMAN GENETIC ORIGIN

<220>

<221> misc_feature

<222> (1045)..(1047)

<223> encodes T2609 residue

<400> 21

tccggtaaag atcctaattc taaagacaac tcagtaggga ttcaattgct	aggcatcg	60
atggccaatg acctgcctcc ctatgaccca cagtgtggca tccagagtag	cgaataacttc	120
caggcttgg tgaataatat gtccttgta agatataaag aagtgtatgc	cgctgcagca	180
gaagttctag gacttatact tcgatatgtt atggagagaa aaaacatact	ggaggagtct	240
ctgtgtgaac tggttgcgaa acaattgaag caacatcaga atactatgga	ggacaagttt	300
atttgtgtct tgaacaaagt gaccaagagc ttccctcctc ttgcagacag	gttcatgaat	360
gctgtgttct ttctgctgcc aaaatttcat ggagtgttga aaacactctg	tctggaggtg	420
gtactttgtc gtgtggaggg aatgacagag ctgtacttcc agttaaagag	caaggacttc	480
gttcaagtca tgagacatag agatgatgaa agacaaaaag tatgtttgga	cataatttat	540
aagatgatgc caaagtaaa accagtagaa ctccgagaac ttctgaaccc	cgttgtggaa	600
ttcgtttccc atccttctac aacatgttagg gaacaaatgt ataatattct	catgtggatt	660
catgataatt acagagatcc agaaagttag acagataatg actcccagga	aatatttaag	720
ttggcaaaag atgtgctgat tcaaggattt atcgatgaga accctggact	tcaattaatt	780
attcgaaatt tctggagcca taaaactagg ttaccttcaa ataccttggca	ccggttgctg	840
gcactaaatt ccttatattc tcctaagata gaagtgcact ttttaagtt	agcaacaaat	900
tttctgctcg aaatgaccag catgagccca gattatccaa accccatgtt	cgagcatcct	960
ctgtcagaat gcgaatttca ggaatatacc attgattctg attggcg	tttccgaact	1020
gttctcactc cgatgtttgt ggagacccag gcctcccagg gcactctcca	gaccgttacc	1080
caggaagggt ccctctcagc tcgctggcca gtggcaggc agataagggc	caccctcagc	1140
cacatgact tcacactgac acagactgca gatgaaagaa gtcatttga	ttggctgacc	1200
gggagcagca ctgaccgcgt ggtcgaccac accagtcctt catctgactc	cttgcgtt	1260
gcccacacaaga ggagtgaaag gttacagaga gcacccttga agtcagtgg	gcctgatttt	1320

<210> 22

<211> 600
<212> DNA
<213> Artificial Sequence

<220>
<223> cDNA sequence encoding the 2500-2700 peptide

<220>
<221> CDS
<222> (1)..(600)
<223> HUMAN GENETIC ORIGIN

<220>
<221> misc_feature
<222> (325)..(327)
<223> encodes T2609 residue

<400> 22

ttggcaaaag atgtgctgat tcaaggattg atcgatgaga accctggact tcaattaatt	60
attcgaaatt tctggagcca tgaaactagg ttaccttcaa ataccttgaa ccgggttgctg	120
gcactaaatt ccttatattc tcctaagata gaagtgcact tttaagttt agcaacaaat	180
tttctgctcg aatgaccag catgagccca gattatccaa accccatgtt cgagcatcct	240
ctgtcagaat gcgaatttca ggaatatacc attgattctg attggcggtt ccgaagtact	300
gttctcaactc cgatgtttgt ggagacccag gcctcccagg gcaactctcca gaccgtacc	360
caggaagggt ccctctcagc tcgctggcca gtggcagggc agataagggc caccagcag	420
cagcatgact tcacactgac acagactgca gatggaagaa gtcatttga ttggctgacc	480
gggagcagca ctgaccgct ggtcgaccac accagtcct catctgactc cttgctgttt	540
gccccacaaga ggagtgaaag gttacagaga gcacccttga agtcagtgg gcctgatttt	600

<210> 23

<211> 1284
<212> DNA
<213> Artificial sequence

<220>
<223> cDNA sequence encoding 2275-2702 peptide

<220>
<221> CDS
<222> (1)..(1284)
<223> HUMAN GENETIC ORIGIN

<220>
<221> misc_feature
<222> (1003)..(1005)
<223> encodes T2609 residue

<400> 23

caattgctag gcacatcgat ggccaaatgac ctgcctccct atgacccaca gtgtggcatc	60
cagagtagcg aataacttcca ggctttggtg aataaatatgt cctttgttaag atataaaagaa	120
gtgtatgccg ctgcagcaga agttcttagga cttatacttc gatatgttat ggagagaaaa	180
aacatactgg aggagtctct gtgtgaactg gttgcgaaac aattgaagca acatcagaat	240
actatggagg acaagtttat tgtgtgcttg aacaaagtga ccaagagctt ccctcccttt	300
gcagacaggt tcatgaatgc tgtgttcttt ctgctgccaa aatttcatgg agtgttggaa	360
acactctgtc tggaggtggt actttgtcgt gtggagggaa tgacagagct gtacttccag	420
ttaaagagca aggacttcgt tcaagtcatg agacatagag atgatgaaag acaaaaagta	480
tgtttggaca taatttataa gatgatgcca aagttaaaac cagtagaact ccgagaactt	540
ctgaaccccg ttgtggaatt cgtttcccat cttctacaa catgtaggaa acaaatgtat	600
aatattctca tgtggattca tgataattac agagatccag aaagtgagac agataatgac	660
tcccaggaaa tatttaagtt ggcaaaagat gtgctgattc aaggattgat cgatgagaac	720
cctggacttc aattaattat tcgaaatttc tggagccatg aaacttaggtt accttcaaatt	780
accttggacc ggttgctggc actaaattcc ttatattctc ctaagataga agtgcacttt	840
ttaagtttag caacaaattt tctgctcgaa atgaccagca tgagcccaga ttatccaaac	900
cccatgttcg agcatcctct gtcagaatgc gaatttcagg aatataccat tgattctgat	960
tggcgtttcc gaagtactgt tctcaactccg atgtttgtgg agacccaggc ctcccaaggc	1020
actctccaga cccgtaccca ggaagggtcc ctctcagctc gctggccagt ggcagggcag	1080
ataagggcca cccagcagca gcatgacttc acactgacac agactgcaga tggaagaagc	1140
tcatttgatt ggctgaccgg gaggcagcact gacccgctgg tcgaccacac cagttccctca	1200
tctgactcct tgctgtttgc ccacaagagg agtgaaggt tacagagagc acccttgaag	1260
tcagtggggc ctgattttgg gaaa	1284

<210> 24

<211> 819

<212> DNA

<213> Artificial Sequence

<220>

<223> cDNA sequence encoding 2429-2072 peptide

<220>

<221> CDS

<222> (1)..(819)

<223> HUMAN GENETIC ORIGIN

<220>

<221> misc_feature

<222> (538)..(540)
<223> encodes T2609 residue

<400> 24

gaaagacaaa aagtatgttt ggacataatt tataagatga tgccaaagt	aaaaccagta	60
gaactccgag aacttctgaa ccccgttgtg gaattcggtt cccatccttc	tacaacatgt	120
agggacaaa tgtataatat tctcatgtgg attcatgata attacagaga	tccagaaagt	180
gagacagata atgactccca gaaaatattt aagttggcaa aagatgtgt	gattcaagga	240
ttgatcgatg agaaccctgg acttcaatta attattcgaa atttctggag	ccatgaaact	300
aggttacctt caaataacctt ggaccgggttg ctggcactaa attccttata	ttctcctaag	360
atagaagtgc acttttaag tttagcaaca aattttctgc tcgaaatgac	cagcatgagc	420
ccagattatc caaaccat gttcgagcat cctctgtcag aatgcgaatt	tcagaaat	480
accattgatt ctgattggcg tttccgaagt actgttctca ctccgatgtt	tgtggagacc	540
caggcctccc agggcactct ccagaccgcgt acccaggaag ggtccctctc	agctcgctgg	600
ccagtggcag ggcagataag ggcacccag cagcagcatg acttcacact	gacacagact	660
gcagatggaa gaagctcatt tgattggctg accggagca gcactgaccc	gctggtcgac	720
cacaccagtc cctcatctga ctcccttgctg tttgcccaca agaggagtga	aaggttacag	780
agagcaccct tgaagtcaagt gggcctgat tttggaaa		819

<210> 25

<211> 420
<212> DNA
<213> Artificial Sequence

<220>
<223> cDNA Sequence encoding 2561-2700 peptide

<220>
<221> CDS
<222> (1)..(420)
<223> HUMAN GENETIC ORIGIN

<220>
<221> misc_feature
<222> (145)..(147)
<223> Encodes T2609 residue

<400> 25

tttctgctcg aaatgaccag catgagccca gattatccaa accccatgtt	cgagcatcct	60
ctgtcagaat gcgaatttca ggaatatacc attgattctg attggcggtt	ccgaagtact	120
gttctcaactc cgatgtttgt ggagacccag gcctcccagg gcactctcca	gaccctgtacc	180

caggaagggt ccctctcagc tcgctggcca gtggcagggc agataaggc caccagcag 240
cagcatgact tcacactgac acagactgca gatggaagaa gtcatttga ttggctgacc 300
gggagcagca ctgaccgct ggtcgaccac accagtcct catctgactc cttgctgttt 360
gcccacaaga ggagtgaaag gttacagaga gcacccttga agtcagtggg gcctgatttt 420

<210> 26

<211> 306
<212> DNA
<213> Artificial Sequence

<220>
<223> cDNA sequence encoding 2600-2702 peptide

<220>
<221> CDS
<222> (1)..(306)
<223> HUMAN GENETIC ORIGIN

<220>
<221> misc_feature
<222> (25)..(27)
<223> Encodes T2609 residue

<400> 26

gttctcaactc cgatgttgt ggagacccag gcctccagg gcactctcca gaccgtacc 60
caggaagggt ccctctcagc tcgctggcca gtggcagggc agataaggc caccagcag 120
cagcatgact tcacactgac acagactgca gatggaagaa gtcatttga ttggctgacc 180
gggagcagca ctgaccgct ggtcgaccac accagtcct catctgactc cttgctgttt 240
gcccacaaga ggagtgaaag gttacagaga gcacccttga agtcagtggg gcctgatttt 300
ggaaaa 306

<210> 27

<211> 34
<212> DNA
<213> Artificial sequence

<220>
<223> Primer to create T2609A mutation

<400> 27

tccgatgttt gtggaggacc aggcctccca gggc 34

<210> 28

<211> 34
<212> DNA

<213> Artificial Sequence

<220>

<223> Reverse primer to create T2609A mutation

<400> 28

gccctggag gcctggcct ccacaaacat cgga

34